# NiceProt View of Swiss-Prot: P27449

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[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

## General information about the entry

| | |
|---|---|
| Entry name | **VATL_HUMAN** |
| Primary accession number | **P27449** |
| Secondary accession numbers | None |
| Entered in Swiss-Prot in | Release 23, August 1992 |
| Sequence was last modified in | Release 23, August 1992 |
| Annotations were last modified in | Release 41, June 2002 |

## Name and origin of the protein

| | |
|---|---|
| Protein name | **Vacuolar ATP synthase 16 kDa proteolipid subunit** |
| Synonym | **EC** 3.6.3.14 |
| Gene name | **ATP6V0C** or **ATP6L** or **ATP6C** or **ATPL** |
| From | Homo sapiens (Human) [TaxID: 9606] |
| Taxonomy | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |

## References

[1] SEQUENCE FROM NUCLEIC ACID.
MEDLINE=91239553; PubMed=1709739; [NCBI, ExPASy, EBI, Israel, Japan]
Gillespie G.A., Somlo S., Gerarano G.G., Wernstat-Sayslow D., Reeders S.T.:
"CpG island in the region of an autosomal dominant polycystic kidney disease locus defines the 5' end of a gene encoding a putative proton channel.":
Proc. Natl. Acad. Sci. U.S.A. 88:4289-4293(1991).

[2] SEQUENCE FROM NUCLEIC ACID.
**TISSUE** Brain, Muscle, and Skin:
Strausberg R.:
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

## Comments

- ***FUNCTION***: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE INTEGRAL V0 COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
- ***CATALYTIC ACTIVITY***: ATP + $H_2O$ + $H^+$(In) = ADP + phosphate + $H^+$(Out).
- ***SUBUNIT***: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B, C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN) WHICH IS PRESENT AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).
- ***SUBCELLULAR LOCATION***: Integral membrane protein. Vacuolar
- ***MISCELLANEOUS***: THIS SUBUNIT BINDS DICYCLOHEXYLCARBODIIMIDE (DCDD) WHICH INHIBITS THE ATPASE.
- ***SIMILARITY***: BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.

## Copyright

## Cross-references

| | |
|---|---|
| EMBL | M62762; AAA60039.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>BC004537; AAH04537.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>BC007389; AAH07389.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>BC007759; AAH07759.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]<br>BC009290; AAH09290.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| PIR | A39367; A39367. |
| Genew | HGNC:855; ATP6V0C. |
| CleanEx | HS_NC_855; ATP6V0C |
| MIM | 108745 [NCBI / EBI]. |
| GeneCards | ATP6V0C. |
| GeneLynx | ATP6V0C; Homo sapiens. |
| SOURCE | ATP6V0C; Homo sapiens. |
| Ensembl | P27449. Homo sapiens. [Entry / Contig view] |
| InterPro | IPR002379; ATPase_Csub.<br>IPR005124; Vac_ATPsynt_Csub.<br>Graphical view of domain structure. |
| Pfam | PF00137; ATP-synt_C; 2. |
| PRINTS | PR00122; VACATPASE. |
| TIGRFAMs | TIGR00310; V_ATP_synt_C; 1. |
| ProDom | [Domain structure / List of sequences sharing at least 1 domain]. |
| BLOCKS | P27449. |
| ProtoNet | 27449. |
| ProtoMap | P27449. |
| PRESAGE | P27449. |
| DIP | 27449. |
| ModBase | P27449. |
| SWISS-2DPAGE | Get region on 2D PAGE. |

## Keywords

Hydrolase; Hydrogen ion transport; ATP synthesis; Transmembrane.

## Features

| Key | From | To | Length | Description |
|---|---|---|---|---|
| DOMAIN | 1 | 10 | 10 | LUMENAL (*POTENTIAL*). |
| TRANSMEM | 11 | 33 | 23 | *POTENTIAL*. |
| DOMAIN | 34 | 55 | 22 | CYTOPLASMIC (*POTENTIAL*). |
| TRANSMEM | 56 | 76 | 21 | *POTENTIAL*. |
| DOMAIN | 77 | 92 | 16 | LUMENAL (*POTENTIAL*). |
| TRANSMEM | 93 | 114 | 22 | *POTENTIAL*. |
| DOMAIN | 115 | 126 | 12 | CYTOPLASMIC (*POTENTIAL*). |
| TRANSMEM | 127 | 152 | 26 | *POTENTIAL*. |
| DOMAIN | 153 | 155 | 3 | LUMENAL (*POTENTIAL*). |
| BINDING | 130 | 139 | | DICYCLOHEXYLCARBODIIMIDE (*POTENTIAL*). |

Feature aligner

Feature table viewer

## Sequence information

Length: **155 AA** Molecular weight: **15736 Da** CRC64 **91141854A0492A5B** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
        |          |          |          |          |          |
MSESKSGPEY ASFFAVMGAS AAMVFSALGA AYGTAKSGTG IAAMSVMRPE QIMKSIIPVV

        70         80         90        100        110        120
        |          |          |          |          |          |
MAGIIAIYGL VVAVLIANSL NDDISLYKSF LQLGAGLSVG LSGLAAGFAI GIVGDAGVRG

       130        140        150
       |          |          |
TAQQPRLFVG MILILIFAEV LGLYGLIVAL ILSTK
```

P27449 in FASTA format

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Direct BLAST submission at EMBnet-CH SIB (Switzerland)

Direct BLAST submission at NCBI (Bethesda, USA)

ScanProsite, MotifScan

Tools

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

Feature table viewer (Java)

Search the SWISS-MODEL Repository

# NiceProt View of Swiss-Prot: P23956

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[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

## General information about the entry

| | |
|---|---|
| Entry name | **VATL_BOVIN** |
| Primary accession number | **P23956** |
| Secondary accession numbers | None |
| Entered in Swiss-Prot in | Release 21, March 1992 |
| Sequence was last modified in | Release 21, March 1992 |
| Annotations were last modified in | Release 41, June 2002 |

## Name and origin of the protein

| | |
|---|---|
| Protein name | **Vacuolar ATP synthase 16 kDa proteolipid subunit** |
| Synonym | **EC** 3.6.3.14 |
| Gene name | **ATP6V0C** or **ATP6L** or **ATP6C** |
| From | Bos taurus (Bovine) [TaxID: 9913] |
| Taxonomy | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. |

## References

[1] SEQUENCE FROM NUCLEIC ACID.
MEDLINE=88289753; PubMed=2456571; [NCBI, ExPASy, EBI, Israel, Japan]
Mandel M., Moriyama Y., Hulmes J.D., Pan Y.-C.E., Nelson H., Nelson N.;
"cDNA sequence encoding the 16-kDa proteolipid of chromaffin granules implies gene duplication in the evolution of H+-ATPases";
Proc. Natl. Acad. Sci. U.S.A. 85:5521-5524(1988).

[2] REVISIONS.
Nelson N.;
Submitted (JUN-1988) to the EMBL/GenBank/DDBJ databases.

[3] SEQUENCE OF 7-26.
**TISSUE**=Brain;
MEDLINE=89338721; PubMed=2527163; [NCBI, ExPASy, EBI, Israel, Japan]
Dermietzel R., Voelker M., Hwang T.K., Berzborn R.L., Meyer H.E.;
"A 16 kDa protein co-isolating with gap junctions from brain tissue belonging to the class of proteolipids of the vacuolar H+-ATPases";
FEBS Lett. 253:1-5(1989).

## Comments

- ***FUNCTION***: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE INTEGRAL V0 COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
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- ***SIMILARITY***: BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.

## Copyright



## Cross-references

| | |
|---|---|
| EMBL | J03835; AAA30397.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] |
| PIR | A31320; PXBOV6.<br>S05209; S05209. |
| InterPro | IPR002379; ATPase_C-sub.<br>IPR000245; Vac_ATPsynt_C-sub.<br>Graphical view of domain structure. |
| Pfam | PF00137; ATP-synt_C; 2. |
| PRINTS | PR00122; VACATPASE. |
| TIGRFAMs | TIGR01100; V_ATP_synt_C; 1. |
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| BLOCKS | P23956. |
| ProtoNet | P23956. |
| ProtoMap | P23956. |
| PRESAGE | P23956. |
| DIP | P23956. |
| ModBase | P23956. |
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| DOMAIN | 1 | 11 | 10 | LUMENAL (*POTENTIAL*). |
| TRANSMEM | 12 | 34 | 23 | *POTENTIAL*. |
| DOMAIN | 35 | 56 | 22 | CYTOPLASMIC (*POTENTIAL*). |
| TRANSMEM | 57 | 77 | 21 | *POTENTIAL*. |
| DOMAIN | 78 | 93 | 16 | LUMENAL (*POTENTIAL*). |
| TRANSMEM | 94 | 115 | 22 | *POTENTIAL*. |
| DOMAIN | 116 | 127 | 12 | CYTOPLASMIC (*POTENTIAL*). |
| TRANSMEM | 128 | 153 | 26 | *POTENTIAL*. |
| DOMAIN | 154 | 155 | 2 | LUMENAL (*POTENTIAL*). |
| BINDING | 123 | 123 | | DICYCLOHEXYLCARBODIIMIDE (*POTENTIAL*). |

Feature aligner

Feature table viewer

## Sequence information

Length: **155 AA** Molecular weight: **15720 Da** CRC64: **326B20B5F7D7D607** [This is a checksum on the sequence]

```
          10         20         30         40         50         60
          |          |          |          |          |          |
MSEAANGPEY ASFFAVMGAS AAMVFSALGA AYGTAKSGTG IAAMSVMRPE MIMKSIIPVV

          70         80         90        100        110        120
          |          |          |          |          |          |
MAGIIAIYGL VVAVLIANSL NDGISLYRSF LQLGAGLSVG LSGLAAGFAI GIVGDAGVRG

         130        140        150
          |          |          |
TAQQPRLFVG MILILIFAEV LGLYGLIVAL ILSTK
```

P23956 in FASTA format

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Direct BLAST submission at EMBnet-CH SIB (Switzerland)


Direct BLAST submission at NCBI (Bethesda, USA)


ScanProsite, MotifScan


Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)


Feature table viewer (Java)


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| L Number | Hits | Search Text | DB | Time stamp |
|---|---|---|---|---|
| 1 | 14 | vacuolar adj atp adj synthase | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:42 |
| 2 | 524 | proteolipid | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:42 |
| 3 | 0 | (vacuolar adj atp adj synthase) near5 proteolipid | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:42 |
| 4 | 0 | (vacuolar adj atp adj synthase) with proteolipid | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:42 |
| 5 | 8 | (vacuolar adj atp adj synthase) and proteolipid | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:43 |
| 6 | 0 | atp6v0c | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:43 |
| 7 | 0 | atp6l | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:43 |
| 8 | 8 | atp6c | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:45 |
| 9 | 14 | vacuolar near3 atpS near3 synthase | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:45 |
| 10 | 4 | vacuolar near3 atpS near3 proteolipid | USPAT; US-PGPUB; EPO; JPO; DERWENT | 2003/02/07 10:46 |